

#21

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the Application of:
Steven R. Wiley

Docket No.: 2968-B

Serial No: 09/742,454

Group Art Unit: 1653

Filed: December 19, 2000

Examiner: Not assigned

For: TWEAK RECEPTOR

RESPONSE TO NOTICE TO COMPLY AND STATEMENT
UNDER 37 C.F.R. §1.821(g)

BOX SEQUENCE LISTING

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

In response to the Notice to Comply dated March 13, 2001 (copy enclosed), a Substitute Sequence Listing, in both paper and computer readable form, is submitted herewith, to correct errors as listed in the Raw Sequence Listing Error Report. Applicant hereby states the contents of the enclosed paper and computer readable copies of the Sequence Listing are identical, and contain no new matter.

Immunex Corporation
Law Department
51 University Street
Seattle, Washington 98101
Telephone: (206) 587-0430

Respectfully submitted,

Joseph R. Baker
Registration No. 40,900

CERTIFICATE OF MAILING

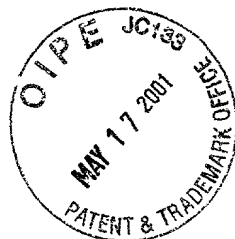
I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: BOX SEQUENCE Assistant Commissioner for Patents, Washington, D.C. 20231, on the date indicated below.

Date: May 14, 2001

Signed: Elizabeth M. McCarthy
Elizabeth M. McCarthy

09742454-054701

#4



SEQUENCE LISTING

<110> WILEY, Steven R.

<120> TWEAK Receptor

<130> 2968-B

<140> US/09/742,454

<141> 2000-12-19

<150> 60/172,878

<151> 1999-12-20

<150> 60/203,347

<151> 2000-05-10

<160> 7

<170> PatentIn Ver. 2.0

<210> 1

<211> 898

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (52)..(873)

<220>

<223> Description of Artificial Sequence: human TWEAK
fusion protein construct

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Met Ala
1

aca ggc tcc cgg acg tcc ctg ctc ctg gct ttt ggc ctg ctc tgc ctg 105
Thr Gly Ser Arg Thr Ser Leu Leu Ala Phe Gly Leu Leu Cys Leu
5 10 15

ccc tgg ctt caa gag ggc agt gca act agt tct gac cgt atg aaa cag 153
Pro Trp Leu Gln Glu Gly Ser Ala Thr Ser Ser Asp Arg Met Lys Gln
20 25 30

ata gag gat aag atc gaa gag atc cta agt aag att tat cat ata gag 201
Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu
35 40 45 50

aat gaa atc gcc cgt atc aaa aag ctg att ggc gag cgg act aga tct 249
Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr Arg Ser
55 60 65

agt ttg ggg agc cgg gca tcg ctg tcc gcc cag gag cct gcc cag gag 297
Ser Leu Gly Ser Arg Ala Ser Leu Ser Ala Gln Glu Pro Ala Gln Glu

102750-43424260

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Glu Leu Val Ala Glu Glu Asp Gln Asp Pro Ser Glu Leu Asn Pro Gln			
85	90	95	
aca gaa gaa agc cag gat cct gcg cct ttc ctg aac cga cta gtt cgg			393
Thr Glu Glu Ser Gln Asp Pro Ala Pro Phe Leu Asn Arg Leu Val Arg			
100	105	110	
cct cgc aga agt gca cct aaa ggc cgg aaa aca cgg gct cga aga gcg			441
Pro Arg Arg Ser Ala Pro Lys Gly Arg Lys Thr Arg Ala Arg Arg Ala			
115	120	125	130
atc gca gcc cat tat gaa gtt cat cca cga cct gga cag gac gga gcg			489
Ile Ala Ala His Tyr Glu Val His Pro Arg Pro Gly Gln Asp Gly Ala			
135	140	145	
cag gca ggt gtg gac ggg aca gtg agt ggc tgg gag gaa gcc aga atc			537
Gln Ala Gly Val Asp Gly Thr Val Ser Gly Trp Glu Glu Ala Arg Ile			
150	155	160	
aac agc tcc agc cct ctg cgc tac aac cgc cag atc ggg gag ttt ata			585
Asn Ser Ser Ser Pro Leu Arg Tyr Asn Arg Gln Ile Gly Glu Phe Ile			
165	170	175	
gtc acc cgg gct ggg ctc tac tac ctg tac tgt cag gtg cac ttt gat			633
Val Thr Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val His Phe Asp			
180	185	190	
gag ggg aag gct gtc tac ctg aag ctg gac ttg ctg gtg gat ggt gtg			681
Glu Gly Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu Val Asp Gly Val			
195	200	205	210
ctg gcc ctg cgc tgc ctg gag gaa ttc tca gcc act gcg gcc agt tcc			729
Leu Ala Leu Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala Ala Ser Ser			
215	220	225	
ctc ggg ccc cag ctc cgc ctc tgc cag gtg tct ggg ctg ttg gcc ctg			777
Leu Gly Pro Gln Leu Arg Leu Cys Gln Val Ser Gly Leu Leu Ala Leu			
230	235	240	
cgg cca ggg tcc tcc ctg cgg atc cgc acc ctc ccc tgg gcc cat ctc			825
Arg Pro Gly Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp Ala His Leu			
245	250	255	
aag gct gcc ccc ttc ctc acc tac ttc gga ctc ttc cag gtt cac tga			873
Lys Ala Ala Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln Val His			
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<210> 2

<211> 273

<212> PRT

<213> Artificial Sequence

<220>
<221> CDS
<222> (52)..(873)

<220>
<223> Description of Artificial Sequence: human TWEAK
fusion protein construct

<400> 2

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			20					25					30			
Lys	Gln	Ile	Glu	Asp	Lys	Ile	Glu	Glu	Ile	Leu	Ser	Lys	Ile	Tyr	His	
		35					40					45				
Ile	Glu	Asn	Glu	Ile	Ala	Arg	Ile	Lys	Lys	Leu	Ile	Gly	Glu	Arg	Thr	
	50					55					60					
Arg	Ser	Ser	Leu	Gly	Ser	Arg	Ala	Ser	Leu	Ser	Ala	Gln	Glu	Pro	Ala	
65					70					75					80	
Gln	Glu	Glu	Leu	Val	Ala	Glu	Glu	Asp	Gln	Asp	Pro	Ser	Glu	Leu	Asn	
				85					90					95		
Pro	Gln	Thr	Glu	Glu	Ser	Gln	Asp	Pro	Ala	Pro	Phe	Leu	Asn	Arg	Leu	
			100					105					110			
Val	Arg	Pro	Arg	Arg	Ser	Ala	Pro	Lys	Gly	Arg	Lys	Thr	Arg	Ala	Arg	
		115					120					125				
Arg	Ala	Ile	Ala	Ala	His	Tyr	Glu	Val	His	Pro	Arg	Pro	Gly	Gln	Asp	
	130					135					140					
Gly	Ala	Gln	Ala	Gly	Val	Asp	Gly	Thr	Val	Ser	Gly	Trp	Glu	Glu	Ala	
145					150					155					160	
Arg	Ile	Asn	Ser	Ser	Ser	Pro	Leu	Arg	Tyr	Asn	Arg	Gln	Ile	Gly	Glu	
			165						170					175		
Phe	Ile	Val	Thr	Arg	Ala	Gly	Leu	Tyr	Tyr	Leu	Tyr	Cys	Gln	Val	His	
			180					185					190			
Phe	Asp	Glu	Gly	Lys	Ala	Val	Tyr	Leu	Lys	Leu	Asp	Leu	Leu	Val	Asp	
		195					200					205				
Gly	Val	Leu	Ala	Leu	Arg	Cys	Leu	Glu	Glu	Phe	Ser	Ala	Thr	Ala	Ala	
	210					215					220					
Ser	Ser	Leu	Gly	Pro	Gln	Leu	Arg	Leu	Cys	Gln	Val	Ser	Gly	Leu	Leu	
225					230					235					240	
Ala	Leu	Arg	Pro	Gly	Ser	Ser	Leu	Arg	Ile	Arg	Thr	Leu	Pro	Trp	Ala	
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09444260

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<211> 868
<212> DNA
<213> Homo sapiens
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<221> CDS
<222> (53) .. (442)
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Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly Leu Trp
5 10 15

ctg gcg ttg ctg cgc tcc gtg gcc ggg gag caa gcg cca ggc acc gcc 154
Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly Thr Ala
20 25 30

ccc tgc tcc cgc ggc agc tcc tgg agc gcg gac ctg gac aag tgc atg 202
Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys Cys Met
35 40 45 50

gac tgc gcg tct tgc agg gcg cga ccg cac agc gac ttc tgc ctg ggc 250
Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys Leu Gly
55 60 65

tgc gct gca gca cct cct gcc ccc ttc cgg ctg ctt tgg ccc atc ctt 298
Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu
70 75 80

ggg ggc gct ctg agc ctg acc ttc gtg ctg ggg ctg ctt tct ggc ttt 346
Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser Gly Phe
85 90 95

ttg	gtc	tgg	aga	cga	tgc	cgc	agg	aga	gag	aag	ttc	acc	acc	ccc	ata	394
Leu	Val	Trp	Arg	Arg	Cys	Arg	Arg	Arg	Glu	Lys	Phe	Thr	Thr	Pro	Ile	
	100					105					110					

gag gag acc ggc gga gag ggc tgc cca gct gtg gcg ctg atc cag tga 442
Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile Gln
115 120 125

caatgtgcc cctgccagcc ggggctcgcc cactcatcat tcattcatcc attctagagc 502

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<211> 932
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<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: human TWEAK
receptor fusion protein construct

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1		5				10				15							
ctc	tgg	ctg	gcg	ttg	ctg	cgc	tcc	gtg	gcc	ggg	gag	caa	gcg	cca	ggc	96	
Leu	Trp	Leu	Ala	Leu	Leu	Arg	Ser	Val	Ala	Gly	Glu	Gln	Ala	Pro	Gly		
			20					25					30				
acc	gcc	ccc	tgc	tcc	cgc	ggc	agc	tcc	tgg	agc	gcg	gac	ctg	gac	aag	144	
Thr	Ala	Pro	Cys	Ser	Arg	Gly	Ser	Ser	Trp	Ser	Ala	Asp	Leu	Asp	Lys		
			35					40					45				
tgc	atg	gac	tgc	gcg	tct	tgc	agg	gcg	cga	ccg	cac	agc	gac	ttc	tgc	192	
Cys	Met	Asp	Cys	Ala	Ser	Cys	Arg	Ala	Arg	Pro	His	Ser	Asp	Phe	Cys		
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ctg	ggc	tgc	gct	gca	gca	cct	cct	gcc	ccc	ttc	cgg	ctg	ctt	tgg	aga	240	
Leu	Gly	Cys	Ala	Ala	Ala	Pro	Pro	Ala	Pro	Phe	Arg	Leu	Leu	Trp	Arg		
65					70					75			80				
tct	tgt	gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	gcc	288	

Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Cys	Pro	Ala	Pro	Glu	Ala		
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gag	ggc	gcg	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	336
Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	
			100					105					110			
ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	384
Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	
			115					120					125			
agc	cac	gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	432
Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	
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gag	gtg	cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	480
Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	
					150					155					160	
acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	528
Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	
				165					170					175		
aat	ggc	aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	576
Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	
				180				185					190			
ccc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	624
Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	
			195				200					205				
cag	gtg	tac	acc	ctg	ccc	cca	tcc	cgg	gag	gag	atg	acc	aag	aac	cag	672
Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	
						215					220					
gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	720
Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	
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gtg	gag	tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	768
Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	
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cct	ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tat	agc	aag	ctc	816
Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	
			260					265					270			
acc	gtg	gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	864
Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	
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<211> 309

<212> PRT

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(930)

<220>

<223> Description of Artificial Sequence: human TWEAK
receptor fusion protein construct

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35 40 45Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
50 55 60Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Arg
65 70 75 80Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
85 90 95Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
100 105 110Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
115 120 125Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
130 135 140Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
145 150 155 160Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
165 170 175Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
180 185 190Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
195 200 205

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

T044460

210

215

220

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
225 230 235 240

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
245 250 255

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
260 265 270

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
275 280 285

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
290 295 300

Leu Ser Pro Gly Lys
305

03743444.054704